



Supplementary information, Fig. S2 Cryo-EM analysis of the cGAS-nucleosome complexes. **a** Representative cryo-EM micrograph of the cGAS-nucleosome complexes. **b** Representative 2D class averages. **c** Gold-standard Fourier shell correlation (FSC) curves of the cGAS-nucleosome complexes. **d** Angular distribution of the particles of the 1:1 cGAS-nucleosome complex (left) and the 2:2 cGAS-nucleosome complex (right). **e** Local resolution maps of the 1:1 cGAS-nucleosome complex. The local resolution of the nucleosome was generated from the half maps of the overall map at a resolution of 3.8 Å, and the local resolution of the cGAS protein was generated from the half maps of the subtracted map at a resolution of 4.7 Å. **f** The cryo-EM data processing workflow.